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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/520,946A

DATE: 06/21/2002

TIME: 14:46:47

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\06212002\H520946A.raw

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JUL 08 2002

SEQUENCE LISTING

TECH CENTER 1600/2900

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BROW, MARY ANN D.

7 LYAMICHEV, VICTOR I.

8 OLIVE, DAVID M.

10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
11 PATHOGENS

13 (iii) NUMBER OF SEQUENCES: 165

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: MEDLEN & CARROLL

17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200

18 (C) CITY: SAN FRANCISCO

19 (D) STATE: CALIFORNIA

20 (E) COUNTRY: UNITED STATES OF AMERICA

21 (F) ZIP: 94104

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/08/520,946A

C--> 31 (B) FILING DATE: 30-Aug-1995

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: CARROLL, PETER G.

36 (B) REGISTRATION NUMBER: 32,837

37 (C) REFERENCE/DOCKET NUMBER: FORS-01756

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 705-8410

41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 2506 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58	ATGAGGGGGA TGCTGCCCT CTTTGAGCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
60	CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
62	GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
64	GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

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66 TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG      300
68 GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC      360
70 GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC      420
72 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCTCCA CCCCAGAGGG      480
74 TACCTCATCA CCCCGGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCCG CCAGTGGGCC      540
76 GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG      600
78 GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCCT CCTCAAGAAC      660
80 CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG      720
82 CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTCGCCAAA      780
84 AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC      840
86 CTCCTCCACG AGTTCCGCCCT TCTGGAAAGC CCAAGGCCCT TGGAGGAGGC CCCCTGGCCC      900
88 CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT GTGGGCCGAT      960
90 CTTCTGGCCC TGGCCGCCG CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA     1020
92 GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG GTTCTCGCCA AAGACCTGAG CGTTCTGGCC     1080
94 CTGAGGGAAG GCCTTGGCCT CCCGCCGGG GACGACCCCA TGCTCCTCGC CTACCTCCTG     1140
96 GACCCTTCCA ACACCAACCC CGAGGGGGTG GCCCGGCGCT ACGGCGGGGA GTGGACGGAG     1200
98 GAGGCGGGGG AGCGGGCCGC CCTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT     1260
100 GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGG AGAGGCCCTT TTCCGCTGTC     1320
102 CTGGCCACAC TGGAGGCCAC GGGGGTGC GC      CTGGACGTGG CCTATCTCAG GGCCTTGTCC     1380
104 CTGGAGGTGG CCAGAGGAGT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCCAC     1440
106 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT     1500
108 CCCGCCATCG GCAAGACGGA GAAGACGGG AAGCGCTCCA CCAGCGCCGC CGTCCTGGAG     1560
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114 CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC     1740
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122 GAGACGCCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCTT GATGCGCCGG     1980
124 GCGGCCAAGA CCATCAACTT CGGGGTCTCT TACGGCATGT CGGCCACCG CCTCTCCAG     2040
126 GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTTCATT AGCGCTACTT TCAGAGCTTC     2100
128 CCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG     2160
130 GAGACCCTCT TCGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG     2220
132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC     2280
134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC     2340
136 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCAAAAG AGAGGGCGGA GGCCGTGGCC     2400
138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCTT GGAGGTGGAG     2460
140 GTGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC      2506
142 (2) INFORMATION FOR SEQ ID NO: 2:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 2496 base pairs
146 (B) TYPE: nucleic acid
147 (C) STRANDEDNESS: double
148 (D) TOPOLOGY: linear
150 (ii) MOLECULE TYPE: DNA (genomic)
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
156 ATGGCGATGC TTCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC      60
158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCTCACCA CCAGCCGCGG CGAACCCGTT     120
160 CAGGCGGTCT ACGGCTTCGC CAAAGCCTC CTAAGGCCCT TGAAGGAGGA CGGGGACGTG     180

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162 GTGGTGGTGG TCTTTGACGC CAAGGCCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC      240
164 AAGGCGGGCC GGGCCCCCACC CCCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG      300
166 TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG      360
168 CTGGCCACCC TGGCCAAGCG GCGGAAAAG GAGGGGTACG AGGTGCGCAT CCTACTGCC      420
170 GACCGCGACC TCTACCAGCT CCTTTCGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC      480
172 CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC      540
174 TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG      600
176 AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG      660
178 GACCGAGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT      720
180 TCCCGGAAGC TTTCCAGGT GCACACTGAC CTGCCCCTGG AGGTGGACTT CGGGAGGCGC      780
182 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGGAGTT TGGAAGCCTC      840
184 CTCCACGAGT TCGGCCTCCT GGAGGGGCGG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT      900
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188 CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC      1020
190 CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG      1080
192 CCGGAGGGCC TGGACCTCTT CCCAGAGGAA GACCCCATGC TCCTGGCCTA CCTTCTGGAC      1140
194 CCCTCCAACA GCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT      1200
196 GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG      1260
198 GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTG      1320
200 GCGCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG      1380
202 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCTGGC CGGCCACCCC      1440
204 TTCAACCTCA ACTCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT      1500
206 GCCATCGGCA AGACGGAGAA GACGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC      1560
208 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC      1620
210 AAGAACACCT ACATAGACCC CCTGCCGCGC CTGGTCCACC CCAAGACCGG CCGGCTCCAC      1680
212 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCACCTG      1740
214 CAGAACATCC CCGTGCACAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG      1800
216 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC      1860
218 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG      1920
220 ACCGCCAGCT GGATGTTTCG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG      1980
222 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG      2040
224 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC      2100
226 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG      2160
228 ACCCTCTTCG GCCGCCGGCG CTATGTGCCG GACCTCAACG CCCGGGTGAA GAGCGTGCGC      2220
230 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG      2280
232 AAGCTGGCCA TGGTGC GGCT TTTCCCCCG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG      2340
234 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT      2400
236 TTGGCCAAGG AGGTATGGA GGGGTCTGG CCCCTGCAGG TGCCCTGGA GGTGGAGGTG      2460
238 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG      2496

240 (2) INFORMATION FOR SEQ ID NO: 3:
242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 2504 base pairs
244 (B) TYPE: nucleic acid
245 (C) STRANDEDNESS: double
246 (D) TOPOLOGY: linear
248 (ii) MOLECULE TYPE: DNA (genomic)
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
254 ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC      60
256 CACCTGGCCT ACCGCACCTT CTTGCGCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG      120

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258 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC 180
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262 GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC 300
264 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC 360
266 GACGTTCTCG CCACCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC 420
268 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCGAG 480
270 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG 540
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276 AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC 720
278 CTCAGGCTCT CTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC 780
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282 GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC 900
284 TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCTCTT CCCGCCCCGA GCCCATGTGG 960
286 GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC 1020
288 TTGGCGGGG TAAAGGACCT CAAGGAGGTC CGGGCCCTCC TCGCCAAGGA CCTCGCCGTC 1080
290 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCATGCT CCTCGCCTAC 1140
292 CTCCTGGACC CCTCCAACAC CACCCCGGAG GGGGTGGCGC GCGCTACGG GGGGGAGTGG 1200
294 ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG 1260
296 CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAATA GCCCCCTCTC 1320
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300 CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG 1440
302 GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAATA GGGTGCTCTT TGACGAGCTT 1500
304 AGGCTTCCCG CTTTGGGGA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG 1560
306 CTGGAGGCC TACGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC 1620
308 ACCAAGCTCA AGAACACCTA CGTGGACCCC TCCCCAAGCC TCGTCCACCC GAGGACGGGC 1680
310 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC 1740
312 CCAACCTGC AGAACATCCC CGTCCGCACC CCTTGGGCC AGAGGATCCG CCGGGCCTTC 1800
314 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC 1860
316 CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC 1920
318 CACACCCAGA CCGCAAGCTG GATGTTCCGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG 1980
320 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
322 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
324 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
326 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
328 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
330 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
332 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
334 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCATATC CCTCGCCGTG CCCCTGGAGG 2460
336 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

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338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 832 amino acids

342 (B) TYPE: amino acid

343 (C) STRANDEDNESS: single

344 (D) TOPOLOGY: linear

346 (ii) MOLECULE TYPE: protein

350 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

352 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu

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355	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala
356				20				25				30	
358	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr
359			35				40				45		
361	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala
362		50					55			60			
364	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
365	65				70					75			80
367	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
368				85				90				95	
370	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala
371				100				105				110	
373	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu
374			115				120				125		
376	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
377		130					135				140		
379	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His
380	145				150					155			160
382	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
383				165				170					175
385	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu
386			180				185					190	
388	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg
389		195					200				205		
391	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu
392		210					215				220		
394	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp
395	225				230					235			240
397	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro
398			245					250				255	
400	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu
401			260					265				270	
403	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe
404		275					280				285		
406	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro
407		290					295			300			
409	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met
410	305				310					315			320
412	Leu	Leu	Ala	Leu	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg
413			325					330				335	
415	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg
416			340					345				350	
418	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu
419		355					360				365		
421	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp
422		370				375				380			
424	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu
425	385				390					395			400

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/08/520,946A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029
Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380
Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396
Seq#:8; Xaa Pos.2,63,109,186,205,209,227,228,233,240,243,244,247,260,290
Seq#:8; Xaa Pos.329,336,340,368,414,417,418,431,551,605,773,794,798,823,833

VERIFICATION SUMMARY

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Input Set : A:\Seqsub2.app

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192
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L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:288
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:320
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:352
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:416
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544
L:1237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:768
L:1273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:784
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:816
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:832